



IFWO

## RAW SEQUENCE LISTING

DATE: 08/27/2004

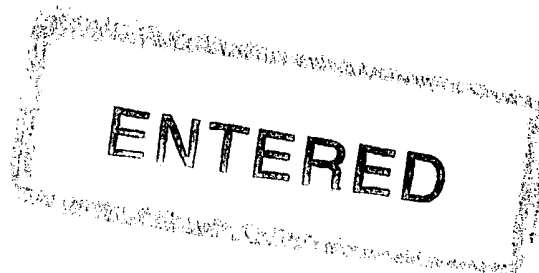
PATENT APPLICATION: US/10/718,000

TIME: 11:39:15

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Output Set: N:\CRF4\08272004\J718000.raw

1 <110> APPLICANT: KRINGELUM, Boerge  
 2 Nilsson, Dan  
 3 SOERENSEN, Kim I.  
 4 <120> TITLE OF INVENTION: METHOD OF IMPROVING THE EFFICACY OF LACTIC ACID BACTERIAL  
 STARTER  
 5 CULTURES AND IMPROVED STARTER CULTURE COMPOSITIONS  
 6 <130> FILE REFERENCE: KRINGELUM=1A  
 7 <140> CURRENT APPLICATION NUMBER: US/10/718,000  
 8 <141> CURRENT FILING DATE: 2003-11-21  
 9 <150> PRIOR APPLICATION NUMBER: US/09/879,036  
 10 <151> PRIOR FILING DATE: 2001-06-13  
 11 <150> PRIOR APPLICATION NUMBER: US 09/086,722  
 12 <151> PRIOR FILING DATE: 1998-05-29  
 13 <150> PRIOR APPLICATION NUMBER: PCT/DK98/00210  
 14 <151> PRIOR FILING DATE: 1998-05-25  
 15 <150> PRIOR APPLICATION NUMBER: US 60/048,337  
 16 <151> PRIOR FILING DATE: 1997-05-30  
 17 <150> PRIOR APPLICATION NUMBER: DK 0633/97  
 18 <151> PRIOR FILING DATE: 1997-05-30  
 19 <160> NUMBER OF SEQ ID NOS: 2  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1638  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Lactococcus lactis  
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 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (255)..(1580)  
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 33 tgacagattt ttttatctaa taattaaaat aattatttca caatgttcac aagcgcttac 180  
 34 aaaagaaaat agattgactt atgctaaact gaataatgta aaaagaattt tacatttaaa 240  
 35 ggagacctat tagt atg aaa atc gta gtt atc ggt aca aac cac gca ggc 290  
 36 Met Lys Ile Val Val Ile Gly Thr Asn His Ala Gly  
 37 1 5 10  
 38 att gct aca gcg aat aca tta ctt gaa caa tat ccc ggg cat gaa att 338  
 39 Ile Ala Thr Ala Asn Thr Leu Leu Glu Gln Tyr Pro Gly His Glu Ile  
 40 15 20 25  
 41 gtc atg att gac cgt aat agc aac atg agt tat cta ggt tgt ggc aca 386  
 42 Val Met Ile Asp Arg Asn Ser Asn Met Ser Tyr Leu Gly Cys Gly Thr  
 43 30 35 40  
 44 gca att tgg gtt gga aga caa att gaa aaa cca gat gaa tta ttt tat 434



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47	gcc aaa gca gag gat ttt gag gca aaa ggg gta aaa att ttg act gaa	482
48	Ala Lys Ala Glu Asp Phe Glu Ala Lys Gly Val Lys Ile Leu Thr Glu	
49	65 70 75	
50	aca gaa gtt tca gaa att gat ttt gct aat aag aaa gtt tat gca aaa	530
51	Thr Glu Val Ser Glu Ile Asp Phe Ala Asn Lys Lys Val Tyr Ala Lys	
52	80 85 90	
53	act aaa tct gat gat gaa ata att gaa gct tac gac aag ctt gtt tta	578
54	Thr Lys Ser Asp Asp Glu Ile Ile Glu Ala Tyr Asp Lys Leu Val Leu	
55	95 100 105	
56	gca aca ggt tca cgt cca att att cct aat cta cca ggc aaa gac ctt	626
57	Ala Thr Gly Ser Arg Pro Ile Ile Pro Asn Leu Pro Gly Lys Asp Leu	
58	110 115 120	
59	aag gga att cat ttt ctg aaa ctt ttt caa gaa ggt caa gca att gac	674
60	Lys Gly Ile His Phe Leu Lys Leu Phe Gln Glu Gly Gln Ala Ile Asp	
61	125 130 135 140	
62	gca gaa ttt gcc aaa gaa aaa gtc aag cgt atc gca gtc att ggt gca	722
63	Ala Glu Phe Ala Lys Glu Lys Val Lys Arg Ile Ala Val Ile Gly Ala	
64	145 150 155	
65	gga tat atc ggt aca gag att gcg gaa gca gct aaa cgt cgg ggt aaa	770
66	Gly Tyr Ile Gly Thr Glu Ile Ala Glu Ala Ala Lys Arg Arg Gly Lys	
67	160 165 170	
68	gaa gtt ctt ctc ttt gac gct gaa aat act tca ctt gca tca tat tat	818
69	Glu Val Leu Leu Phe Asp Ala Glu Asn Thr Ser Leu Ala Ser Tyr Tyr	
70	175 180 185	
71	gat gaa gaa ttt gcc aaa gga atg gat gaa aac ctt gct caa cat gga	866
72	Asp Glu Glu Phe Ala Lys Gly Met Asp Glu Asn Leu Ala Gln His Gly	
73	190 195 200	
74	att gaa ctt cat ttt gga caa ctg gcc aaa gaa ttt aaa gcg aat gag	914
75	Ile Glu Leu His Phe Gly Gln Leu Ala Lys Glu Phe Lys Ala Asn Glu	
76	205 210 215 220	
77	gaa ggt tat gta tca caa atc gta acc aac aag gcg act tat gat gtt	962
78	Glu Gly Tyr Val Ser Gln Ile Val Thr Asn Lys Ala Thr Tyr Asp Val	
79	225 230 235	
80	gat ctt gtc atc aat tgt att ggt ttt act gcc aac agt gcc ttg gca	1010
81	Asp Leu Val Ile Asn Cys Ile Gly Phe Thr Ala Asn Ser Ala Leu Ala	
82	240 245 250	
83	agt gat aag tta gct acc ttc aaa aat ggc gca atc aag gtg gat aag	1058
84	Ser Asp Lys Leu Ala Thr Phe Lys Asn Gly Ala Ile Lys Val Asp Lys	
85	255 260 265	
86	cat caa caa agt agt gat cca gat gtt tac gcg gta ggt gat gtt gcg	1106
87	His Gln Gln Ser Ser Asp Pro Asp Val Tyr Ala Val Gly Asp Val Ala	
88	270 275 280	
89	aca att tat tct aat gcc ttg caa gat ttt act tat atc gct ctt gcc	1154
90	Thr Ile Tyr Ser Asn Ala Leu Gln Asp Phe Thr Tyr Ile Ala Leu Ala	
91	285 290 295 300	
92	tca aac gct gtt cgg tca gga att gtc gca gga cac aat att ggt gga	1202
93	Ser Asn Ala Val Arg Ser Gly Ile Val Ala Gly His Asn Ile Gly Gly	

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Input Set : N:\Crif3\RULE60\10718000.raw

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97          320          325          330
98  ttt ggt tac aat atg act tct aca gga ctt tct gtt aaa gct gct aaa 1298
99  Phe Gly Tyr Asn Met Thr Ser Thr Gly Leu Ser Val Lys Ala Ala Lys
100          335          340          345
101  aaa tta ggt tta gaa gtt tca ttt agt gat ttt gaa gat aaa caa aaa 1346
102  Lys Leu Gly Leu Glu Val Ser Phe Ser Asp Phe Glu Asp Lys Gln Lys
103          350          355          360
104  gct tgg ttt ctt cat gaa aac aac gat agt gtg aaa att cgt atc gta 1394
105  Ala Trp Phe Leu His Glu Asn Asn Asp Ser Val Lys Ile Arg Ile Val
106          365          370          375          380
107  tat gag aca aaa agt cgc aga att att gga gca caa ctt gct agt aaa 1442
108  Tyr Glu Thr Lys Ser Arg Arg Ile Ile Gly Ala Gln Leu Ala Ser Lys
109          385          390          395
110  agt gag ata att gca gga aat ata aat atg ttc agt tta gcg att caa 1490
111  Ser Glu Ile Ile Ala Gly Asn Ile Asn Met Phe Ser Leu Ala Ile Gln
112          400          405          410
113  gag aaa aaa aca att gat gaa cta gct ttg ctt gat tta ttc ttt ctc 1538
114  Glu Lys Lys Thr Ile Asp Glu Leu Ala Leu Leu Asp Leu Phe Phe Leu
115          415          420          425
116  ccc cac ttc aac agt cca tat aat tat atg aca gtt gca gct 1580
117  Pro His Phe Asn Ser Pro Tyr Asn Tyr Met Thr Val Ala Ala
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123 <212> TYPE: PRT
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129          20          25          30
130  Arg Asn Ser Asn Met Ser Tyr Leu Gly Cys Gly Thr Ala Ile Trp Val
131          35          40          45
132  Gly Arg Gln Ile Glu Lys Pro Asp Glu Leu Phe Tyr Ala Lys Ala Glu
133          50          55          60
134  Asp Phe Glu Ala Lys Gly Val Lys Ile Leu Thr Glu Thr Glu Val Ser
135          65          70          75          80
136  Glu Ile Asp Phe Ala Asn Lys Lys Val Tyr Ala Lys Thr Lys Ser Asp
137          85          90          95
138  Asp Glu Ile Ile Glu Ala Tyr Asp Lys Leu Val Leu Ala Thr Gly Ser
139          100          105          110
140  Arg Pro Ile Ile Pro Asn Leu Pro Gly Lys Asp Leu Lys Gly Ile His
141          115          120          125
142  Phe Leu Lys Leu Phe Gln Glu Gly Gln Ala Ile Asp Ala Glu Phe Ala
143          130          135          140

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147                      165                      170                      175
148      Phe Asp Ala Glu Asn Thr Ser Leu Ala Ser Tyr Tyr Asp Glu Glu Phe
149                      180                      185                      190
150      Ala Lys Gly Met Asp Glu Asn Leu Ala Gln His Gly Ile Glu Leu His
151                      195                      200                      205
152      Phe Gly Gln Leu Ala Lys Glu Phe Lys Ala Asn Glu Glu Gly Tyr Val
153                      210                      215                      220
154      Ser Gln Ile Val Thr Asn Lys Ala Thr Tyr Asp Val Asp Leu Val Ile
155      225                      230                      235                      240
156      Asn Cys Ile Gly Phe Thr Ala Asn Ser Ala Leu Ala Ser Asp Lys Leu
157                      245                      250                      255
158      Ala Thr Phe Lys Asn Gly Ala Ile Lys Val Asp Lys His Gln Gln Ser
159                      260                      265                      270
160      Ser Asp Pro Asp Val Tyr Ala Val Gly Asp Val Ala Thr Ile Tyr Ser
161      275                      280                      285
162      Asn Ala Leu Gln Asp Phe Thr Tyr Ile Ala Leu Ala Ser Asn Ala Val
163      290                      295                      300
164      Arg Ser Gly Ile Val Ala Gly His Asn Ile Gly Gly Lys Glu Leu Glu
165      305                      310                      315                      320
166      Ser Val Gly Val Gln Gly Ser Asn Gly Ile Ser Ile Phe Gly Tyr Asn
167                      325                      330                      335
168      Met Thr Ser Thr Gly Leu Ser Val Lys Ala Ala Lys Lys Leu Gly Leu
169                      340                      345                      350
170      Glu Val Ser Phe Ser Asp Phe Glu Asp Lys Gln Lys Ala Trp Phe Leu
171                      355                      360                      365
172      His Glu Asn Asn Asp Ser Val Lys Ile Arg Ile Val Tyr Glu Thr Lys
173      370                      375                      380
174      Ser Arg Arg Ile Ile Gly Ala Gln Leu Ala Ser Lys Ser Glu Ile Ile
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176      Ala Gly Asn Ile Asn Met Phe Ser Leu Ala Ile Gln Glu Lys Lys Thr
177                      405                      410                      415
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180      Ser Pro Tyr Asn Tyr Met Thr Val Ala Ala
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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/27/2004  
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Input Set : N:\Crf3\RULE60\10718000.raw  
Output Set: N:\CRF4\08272004\J718000.raw

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**VERIFICATION SUMMARY**

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TIME: 11:39:16

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Output Set: N:\CRF4\08272004\J718000.raw

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